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OICE

RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/09/625,573

TIME: 14:00:12

Input Set : N:\Crif3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: Charo, Israel

5 Coughlin, Shaun

7 (ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

8 PROTEIN RECEPTORS

10 (iii) NUMBER OF SEQUENCES: 14

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

14 (B) STREET: 5 Palo Alto Square

15 (C) CITY: Palo Alto

16 (D) STATE: California

17 (E) COUNTRY: USA

18 (F) ZIP: 94306-2155

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/625,573

C--> 28 (B) FILING DATE: 25-Jul-2000

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: US/08/446,669

33 (B) FILING DATE: May 25, 1995

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Neeley, Richard

38 (B) REGISTRATION NUMBER: 30,092

39 (C) REFERENCE/DOCKET NUMBER: UCAL-237/01US

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415-843-5000

43 (B) TELEFAX: 415-857-0663

44 (C) TELEX: 380816CooleyPA

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 2232 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: cDNA

56 (iii) HYPOTHETICAL: NO

58 (iv) ANTI-SENSE: NO

ENTERED

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60      (ix) FEATURE:
61          (A) NAME/KEY: CDS
62          (B) LOCATION: 40..1161
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64      GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT      54
65                                     Met Leu Ser Thr Ser
66                                     1      5
67      CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC      102
68      Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr
69      10      15      20
70      ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG      150
71      Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val
72      25      30      35
73      AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC      198
74      Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
75      40      45      50
76      ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC      246
77      Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn
78      55      60      65
79      TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC      294
80      Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala
81      70      75      80      85
82      ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT      342
83      Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser
84      90      95      100
85      GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA      390
86      Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr
87      105      110      115
88      GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC      438
89      Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu
90      120      125      130
91      CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA      486
92      Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu
93      135      140      145
94      AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG      534
95      Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
96      150      155      160      165
97      TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC      582
98      Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys
99      170      175      180
100     CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA      630
101     Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly
102     185      190      195
103     TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG      678
104     Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu
105     200      205      210
106     CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG      726
107     Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu
108     215      220      225

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128	CTT	CGG	TGT	CGA	AAC	GAG	AAG	AAG	AGG	CAT	AGG	GCA	GTG	AGA	GTC	ATC	774
129	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Val	Ile	
130	230					235						240				245	
132	TTC	ACC	ATC	ATG	ATT	GTT	TAC	TTT	CTC	TTC	TGG	ACT	CCC	TAT	AAC	ATT	822
133	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Thr	Pro	Tyr	Asn	Ile	
134						250						255				260	
136	GTC	ATT	CTC	CTG	AAC	ACC	TTC	CAG	GAA	TTC	TTC	GGC	CTG	AGT	AAC	TGT	870
137	Val	Ile	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Ser	Asn	Cys	
138						265						270				275	
140	GAA	AGC	ACC	AGT	CAA	CTG	GAC	CAA	GCC	ACG	CAG	GTG	ACA	GAG	ACT	CTT	918
141	Glu	Ser	Thr	Ser	Gln	Leu	Asp	Gln	Ala	Thr	Gln	Val	Thr	Glu	Thr	Leu	
142						280										290	
144	GGG	ATG	ACT	CAC	TGC	TGC	ATC	AAT	CCC	ATC	ATC	TAT	GCC	TTC	GTT	GGG	966
145	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	
146						295										305	
148	GAG	AAG	TTC	AGA	AGC	CTT	TTT	CAC	ATA	GCT	CTT	GGC	TGT	AGG	ATT	GCC	1014
149	Glu	Lys	Phe	Arg	Ser	Leu	Phe	His	Ile	Ala	Leu	Gly	Cys	Arg	Ile	Ala	
150	310					315						320				325	
152	CCA	CTC	CAA	AAA	CCA	GTG	TGT	GGA	GGT	CCA	GGA	GTG	AGA	CCA	GGA	AAG	1062
153	Pro	Leu	Gln	Lys	Pro	Val	Cys	Gly	Gly	Pro	Gly	Val	Arg	Pro	Gly	Lys	
154						330						335				340	
156	AAT	GTG	AAA	GTG	ACT	ACA	CAA	GGA	CTC	CTC	GAT	GGT	CGT	GGA	AAA	GGA	1110
157	Asn	Val	Lys	Val	Thr	Thr	Gln	Gly	Leu	Leu	Asp	Gly	Arg	Gly	Lys	Gly	
158						345						350				355	
160	AAG	TCA	ATT	GGC	AGA	GCC	CCT	GAA	GCC	AGT	CTT	CAG	GAC	AAA	GAA	GGA	1158
161	Lys	Ser	Ile	Gly	Arg	Ala	Pro	Glu	Ala	Ser	Leu	Gln	Asp	Lys	Glu	Gly	
162						360										370	
164	GCC	TAGAGACAGA	AATGACAGAT	CTCTGCTTTG	GAAATCACAC	GTCTGGCTTC											1211
165	Ala																
167	ACAGATGTGT	GATTACACAGT	GTGAATCTTG	GTGTCTACGT	TACCAGGCAG	GAAGGCTGAG											1271
169	AGGAGAGAGA	CTCCAGCTGG	GTTGGAAAAC	AGTATTTTCC	AAACTACCTT	CCAGTTCCTC											1331
171	ATTTTTGAAT	ACAGGCATAG	AGTTCAGACT	TTTTTTAAAT	AGTAAAAATA	AAATTAAAGC											1391
173	TGAAAACCTGC	AACTTGTAAG	TGTGGTAAAG	AGTTAGTTTG	AGTTGCTATC	ATGTCAAACG											1451
175	TGAAAATGCT	GTATTAGTCA	CAGAGATAAT	CTAGCTTTG	AGCTTAAGAA	TTTTGAGCAG											1511
177	GTGGTATGTT	TGGGAGACTG	CTGAGTCAAC	CCAATAGTTG	TTGATTGGCA	GGAGTTGGAA											1571
179	GTGTGTGATC	TGTGGGCACA	TTAGCCTATG	TGCATGCAGC	ATCTAAGTAA	TGATGTCGTT											1631
181	TGAATCACAG	TATACGCTCC	ATCGCTGTCA	TCTCAGCTGG	ATCTCCATTC	TCTCAGGCTT											1691
183	GCTGCCAAAA	GCCTTTTGTG	TTTTGTTTTG	TATCATTATG	AAGTCATGCG	TTTAATCACA											1751
185	TTGAGTGTGTT	TCAGTGCTTC	GCAGATGTCC	TTGATGCTCA	TATTGTTCCC	TAATTTGCCA											1811
187	GTGGGAACCTC	CTAAATCAAA	TTGGCTTCTA	ATCAAAGCTT	TTAAACCCTA	TTGGTAAAGA											1871
189	ATGGAAGGTG	GAGAAGCTCC	CTGAAGTAAG	CAAAGACTTT	CCTCTTAGTC	GAGCCAAGTT											1931
191	AAGAATGTTT	TTATGTTGCC	CAGTGTGTTT	CTGATCTGAT	GCAAGCAAGA	AACACTGGGC											1991
193	TTCTAGAACC	AGGCAACTTG	GGAAGTAGAC	TCCAAGCTG	GACTATGGCT	CTACTTTCAG											2051
195	GCCACATGGC	TAAAGAAGGT	TTCAGAAAGA	AGTGGGGACA	GAGCAGAACT	TTCACCTTCA											2111
197	TATATTTGTA	TGATCCTAAT	GAATGCATAA	AATGTTAAGT	TGATGGTGAT	GAAATGTAAA											2171
199	TACTGTTTTT	AACAACATATG	ATTTGGAAAA	TAAATCAATG	CTATAACTAT	GTTGATAAAA											2231
201	G																2232
204	(2)	INFORMATION	FOR	SEQ	ID	NO:	2:										
206	(1)	SEQUENCE	CHARACTERISTICS:														

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207      (A) LENGTH: 374 amino acids
208      (B) TYPE: amino acid
209      (D) TOPOLOGY: linear
211      (ii) MOLECULE TYPE: protein
213      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
216 Met  Leu  Ser  Thr  Ser  Arg  Ser  Arg  Phe  Ile  Arg  Asn  Thr  Asn  Glu  Ser
217   1      5      10      15
219 Gly  Glu  Glu  Val  Thr  Thr  Phe  Phe  Asp  Tyr  Asp  Tyr  Gly  Ala  Pro  Cys
220      20      25      30
222 His  Lys  Phe  Asp  Val  Lys  Gln  Ile  Gly  Ala  Gln  Leu  Leu  Pro  Pro  Leu
223      35      40      45
225 Tyr  Ser  Leu  Val  Phe  Ile  Phe  Gly  Phe  Val  Gly  Asn  Met  Leu  Val  Val
226      50      55      60
228 Leu  Ile  Leu  Ile  Asn  Cys  Lys  Lys  Leu  Lys  Cys  Leu  Thr  Asp  Ile  Tyr
229  65      70      75      80
231 Leu  Leu  Asn  Leu  Ala  Ile  Ser  Asp  Leu  Leu  Phe  Leu  Ile  Thr  Leu  Pro
232      85      90      95
234 Leu  Trp  Ala  His  Ser  Ala  Ala  Asn  Glu  Trp  Val  Phe  Gly  Asn  Ala  Met
235      100     105     110
237 Cys  Lys  Leu  Phe  Thr  Gly  Leu  Tyr  His  Ile  Gly  Tyr  Phe  Gly  Gly  Ile
238      115     120     125
240 Phe  Phe  Ile  Ile  Leu  Leu  Thr  Ile  Asp  Arg  Tyr  Leu  Ala  Ile  Val  His
241      130     135     140
243 Ala  Val  Phe  Ala  Leu  Lys  Ala  Arg  Thr  Val  Thr  Phe  Gly  Val  Val  Thr
244 145     150     155     160
246 Ser  Val  Ile  Thr  Trp  Leu  Val  Ala  Val  Phe  Ala  Ser  Val  Pro  Gly  Ile
247      165     170     175
249 Ile  Phe  Thr  Lys  Cys  Gln  Lys  Glu  Asp  Ser  Val  Tyr  Val  Cys  Gly  Pro
250      180     185     190
252 Tyr  Phe  Pro  Arg  Gly  Trp  Asn  Asn  Phe  His  Thr  Ile  Met  Arg  Asn  Ile
253      195     200     205
255 Leu  Gly  Leu  Val  Leu  Pro  Leu  Leu  Ile  Met  Val  Ile  Cys  Tyr  Ser  Gly
256      210     215     220
258 Ile  Leu  Lys  Thr  Leu  Leu  Arg  Cys  Arg  Asn  Glu  Lys  Lys  Arg  His  Arg
259 225     230     235     240
261 Ala  Val  Arg  Val  Ile  Phe  Thr  Ile  Met  Ile  Val  Tyr  Phe  Leu  Phe  Trp
262      245     250     255
264 Thr  Pro  Tyr  Asn  Ile  Val  Ile  Leu  Leu  Asn  Thr  Phe  Gln  Glu  Phe  Phe
265      260     265     270
267 Gly  Leu  Ser  Asn  Cys  Glu  Ser  Thr  Ser  Gln  Leu  Asp  Gln  Ala  Thr  Gln
268      275     280     285
270 Val  Thr  Glu  Thr  Leu  Gly  Met  Thr  His  Cys  Cys  Ile  Asn  Pro  Ile  Ile
271      290     295     300
273 Tyr  Ala  Phe  Val  Gly  Glu  Lys  Phe  Arg  Ser  Leu  Phe  His  Ile  Ala  Leu
274 305     310     315     320
276 Gly  Cys  Arg  Ile  Ala  Pro  Leu  Gln  Lys  Pro  Val  Cys  Gly  Gly  Pro  Gly
277      325     330     335
279 Val  Arg  Pro  Gly  Lys  Asn  Val  Lys  Val  Thr  Thr  Gln  Gly  Leu  Leu  Asp
280      340     345     350

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282 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
283           355           360           365
285 Gln Asp Lys Glu Gly Ala
286           370
289 (2) INFORMATION FOR SEQ ID NO: 3:
291     (i) SEQUENCE CHARACTERISTICS:
292         (A) LENGTH: 1979 base pairs
293         (B) TYPE: nucleic acid
294         (C) STRANDEDNESS: single
295         (D) TOPOLOGY: linear
297     (ii) MOLECULE TYPE: cDNA
299     (iii) HYPOTHETICAL: NO
301     (iv) ANTI-SENSE: NO
303     (ix) FEATURE:
304         (A) NAME/KEY: CDS
305         (B) LOCATION: 81..1160
307     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
310 CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT      60
312 TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC      110
313           Met Leu Ser Thr Ser Arg Ser Arg Phe Ile
314           1           5           10
316 AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT      158
317 Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr
318           15           20           25
320 GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC      206
321 Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala
322           30           35           40
324 CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG      254
325 Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val
326           45           50           55
328 GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG      302
329 Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys
330           60           65           70
332 TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT      350
333 Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu
334           75           80           85           90
336 TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG      398
337 Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp
338           95           100           105
340 GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC      446
341 Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile
342           110           115           120
344 GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA      494
345 Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg
346           125           130           135
348 TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC      542
349 Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val
350           140           145           150
352 ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT      590

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09625573.raw

Output Set: N:\CRF4\10032002\I625573.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:856 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9

L:874 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10